

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTTAAACCAGGGGATGGTGGACACCGCAAAGAAGAAGTCTTGGCGGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACTTGTTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTTT

0906736-07100

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFVCVKTLLKVVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSILRNETHSICTACDESCKTCSGLTNRDCGECEVGWVLDE
GACVDVDECAAEPFPCSAQAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAECT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCTGAGCAGCATGGCCCCGGAGGAGCGCCTTC
CCTGCCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
TAGGATTTGAAGAAGATATCCTGATTGTTTTAGAGGGGAAAATGGCACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTGGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTTCTCAAACACCTCAAATGCTATCT
TCTTTAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG
GATTTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTTCTACCTTGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCCCAACCCCTGTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACAT
GGAACCTGCCATGAACCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTAAACCTTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTTAAAGTTTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTTTCTTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTAAAAATTTTCAAGTGTGTAGTTGGCAGATATTTTCAAATTAACAATGCATTTATGGT
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAAGTTAATGTTGAAGTTACAGCATTTCAGATTTTATTGTCAGATATTTAGAT
GTTTGTACATTTTTTAAAAATTTGCTCTTAATTTTTTAAACTCTCAATACAATATATTTTGACC
TTACCATTATTCCAGAGATTCAGTATTAAAAAATAAATAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGTCAT
TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAATAAATAA
AAAAAATAAATAAATAAATAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

700720"9E2050

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094

><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGC
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTFPYGGKICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCCKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEEERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

T00F20"9E220550

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADD
ALPYLGAIICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 6

FIGURE 7

AGGCTCCTTGGCCCTTTTTCCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCTGGGGCAAGCGCCAGGCCACTGCCCCTGCGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATAACAAGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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T00T20"9E220650

[illegible]

GCTGCTTGCCTGTTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACCTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCCTGGTTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPSSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

090720"GE220557

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTTACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTTCATGGCCTTTCACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCCTTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCGCCTCCC
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTCACCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTCAGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTGTTGTTGTTTTCAGGAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCC
CGGAATAAAACCATTTCCTGC

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FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLGKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMATFTRQGRPRQASRSRQONQREAHFIKRLYQGQLPFPNHA EKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

0590230-012000

[illegible]

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
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FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNISISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNMLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGGERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYAVEDTICSEATTHASYLNNGSNTASSHEQTTSMSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWKYNRGRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FOOTNOTES

FIGURE 14

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC
TCGCTTCCCAGGCGCCGCGGCTGCAGCCTTGCCCCCTTTGCTCGCCTTGAAAATGGAAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCTCTCCCTGCCGAGGCCAGGGAGCGGTACGTGGGAGGTCCATCT
CTAGGGGCGAGACACGCTCGGACCCACCCGACAGCGGCCCTTTGAGAGATTCTGTGAGAAACAAGCGGGCAGACC
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTTCATCGTGGACA
TCTTGCAATTCTTGGACATTGGTCCCTGATGTCAACCCGAGTGGGCCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTTCTCAGAAGCAGAGGGGGCCCCGGCCCCCTGA
GGGAGAATGTGCCACGGGTCTATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAAATTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAAACAAGGCTACATTTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT
GTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACACGGATGTGAAC
ATGAGTGTGTAAATGTGATGGCTCTTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAAA
CGTGACACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTTCTTCGTCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCTCT
GTGTCAACATGGACAGATCCTTTGCCTGTGAGTGTCTTGGAGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
CAAAATTGGACTCTTTGTGCTCTGGGGGACCACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGT
GCCAGTGCTTTGAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCGAGTGCTTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCGAACACATTTGTGTTA
ATAATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGAAGAAAT
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCTG
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT
ATTCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTTACCCAAG
GAGAAGGGGCCAGGCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCGACGGACGGGCTCAGGATG
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAACCTACAAGAGATTGCCTCTGAGCCCAAAACAAGCATCTCTTCTATGCCGAAGACTTCAGCACAAATGG
ATGAGATAAGTGAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACCTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAAACGAAGAAGTAAGAAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAAGCCC
TGAAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGACAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAACAATCAGTACTGA
GAAACCTGGTTTGGCCACAGAACAAAGACAAGAAGTATACACTAATTTGTATAAATTTATCTAGGAAAAAATCCT
TCAGAATTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC
AACTTGCTTCTGCCTCATCTGCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTT
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTTGTAAGTGGACTTTACCTTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAAAATTCACCACTTCAG

FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFI
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KRMRLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINICALNKP
GCEHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGLI
NEDLKTC SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCE
HSCVSSDSFVCQCFEGYILREDGKTCRRKDVCAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPTVITINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

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[illegible]

Signal peptide:

Transmembrane domain:

N-glycosylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

[illegible][illegible]

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTTTGGAACTACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCCGGCTGGGA
CAAGAAGCCGCCGCTGCTGCCCGGGCCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCCGTAAGGCGCTACTATATAAGGCTGCCCGCCCCGAG
CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGGAAGTGGCGCGGGGC
CAGAGCGCGCACAGTTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGGCCACTTGGAATCTGACATGTTCTCTTCCGCCCTGGAGACCGACAGCATG
GACCCATTTGGGCTTGTACCCGACTGGAGGCGGTGAGGAGTCCCAGCTTTGAGAAGTAACT
GAGACCATGCCCCGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTAGAGTTTTCCATTGGCAGTGCCAGTTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTTAATTTTCAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC
CTGAGGCCAGTTCTGTGATGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCCAGCACTTGGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATTTATGTATGTAAGTGAGGTTTG
TTTTGTATATTAAATGGAGTTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHVSRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATAACAATGAATACAAAAACTGGAAGT
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG
CCGCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

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Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	Male	10	0	20
Marital Status	Married	15	0	30
Education	High School	5	0	10
Occupation	Unemployed	10	0	20
Income	\$15,000	\$10,000	\$0	\$40,000
Health Status	Good	15	0	30
Smoking	Non-smoker	10	0	20
Alcohol	Non-drinker	10	0	20
Exercise	Regular	10	0	20
Stress	Low	10	0	20
Sleep	7-8 hours	10	0	20
Diet	Healthy	10	0	20
Family Size	2-3 children	10	0	20
Neighborhood	Urban	10	0	20
Transportation	Car	10	0	20
Insurance	Health	10	0	20
Religion	Christian	10	0	20
Politics	Conservative	10	0	20
Values	Traditional	10	0	20
Attitudes	Positive	10	0	20
Beliefs	Religious	10	0	20
Opinions	Pro-life	10	0	20
Preferences	Conservative	10	0	20
Interests	Religion	10	0	20
Hobbies	Reading	10	0	20
Skills	Basic	10	0	20
Knowledge	General	10	0	20
Wisdom	Common	10	0	20
Experience	Life	10	0	20
Understanding	Human	10	0	20
Empathy	High	10	0	20
Compassion	Deep	10	0	20
Kindness	True	10	0	20
Generosity	High	10	0	20
Humility	Deep	10	0	20
Patience	High	10	0	20
Forgiveness	Deep	10	0	20
Gratitude	High	10	0	20
Optimism	High	10	0	20
Positivity	High	10	0	20
Resilience	High	10	0	20
Strength	High	10	0	20
Courage	High	10	0	20
Determination	High	10	0	20
Perseverance	High	10	0	20
Endurance	High	10	0	20
Stamina	High	10	0	20
Energy	High	10	0	20
Vitality	High	10	0	20
Health	Good	10	0	20
Wellness	Good	10	0	20
Balance	Good	10	0	20
Harmony	Good	10	0	20
Peace	Good	10	0	20
Love	Good	10	0	20
Kindness	Good	10	0	20
Generosity	Good	10	0	20
Humility	Good	10	0	20
Patience	Good	10	0	20
Forgiveness	Good	10	0	20
Gratitude	Good	10	0	20
Optimism	Good	10	0	20
Positivity	Good	10	0	20
Resilience	Good	10	0	20
Strength	Good	10	0	20
Courage	Good	10	0	20
Determination	Good	10	0	20
Perseverance	Good	10	0	20
Endurance	Good	10	0	20
Stamina	Good	10	0	20
Energy	Good	10	0	20
Vitality	Good	10	0	20
Health	Good	10	0	20
Wellness	Good	10	0	20
Balance	Good	10	0	20
Harmony	Good	10	0	20
Peace	Good	10	0	20
Love	Good	10	0	20
Kindness	Good	10	0	20
Generosity	Good	10	0	20
Humility	Good	10	0	20
Patience	Good	10	0	20
Forgiveness	Good	10	0	20
Gratitude	Good	10	0	20
Optimism	Good	10	0	20
Positivity	Good	10	0	20
Resilience	Good	10	0	20
Strength	Good	10	0	20
Courage	Good			

Signal peptide:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCAT
CATGCTGCTATTCTTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTGGACAATG
CAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAAACTTTGTGGTTCTATGGCATTTCATCA
TTTGACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
TGGAATCCTTAAGGGCCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCCTACAGACTAACAATATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAGTCACCAAT
ATTAATGTAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGA
ACTGCCTGAAAAATGTCTGTCCGAAGTGAAGCACTTACAAGAAGCTCTATATTAATCACAACT
TGCTTTCTACAATTTACCTGGAGCCTTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT
TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
GGACTGGAAAACCTTAGAAAGCATCTCTTTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTTGATCTAAATAAAAATCCTATTAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAATATGCCT
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
TACTAACAACCCTAGATTGTCTTACATTCACCCCAATGCATTTTTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTTCATGGAGCCAGATTCAGTGTGTTGCGTGGACC
CACCTGAATTCCAAGGTCAGAATGTTTCGGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTTCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCCCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTCTTGCCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAAATGGCGTAACTCCCAAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATTTAAATAAGAGATATTACAGGCCAATTACAGTTTTTGGTGTCTGGAAGCA
AGTTCTAAATTTCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATTTCTCA
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAA
TGTGTAAATGTCACCACCAAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
AGAAAAAAGTACATCACTGAAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCACCAAGGAAACCTACTCCAAAATGAAC

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FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSPNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGGQNVVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPPQPEIYWITPSGQKLLPNTLTDFYVHSEGLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

0902736-071001

FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCACCTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATTAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTTCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCAAGTTTTTTTTGAATTATGCCACTGCTGAACTTTTAAACAAACACTACAACA
TAAATAATTTGAGTTTtagtgatccaccccttaattgtaccccgatgggtatatTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAGCAAATAAAAGCTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

099276.0700

FIGURE 28

MNLVDLWLTRSLMCLLLQSFLMILCFHSASMC PKGCLCSSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNR
IQSVHKNAFNNLKARARIANNPW HCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
NAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

090279-0700T

[illegible]

ACCGAGCCGAGCGGACCGCAAGGCCGCGCCCGAGATGCAGGTTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGGCCCCCTCCTTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTTCAGGCTCGGCCACGGGCTGCCCGCCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACC GCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCCGGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT
CGTTATCCTACTGGACTACATGTTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACGAGGCGCTGTCCCACCTGCACGGCCT
CATCGTCTTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGAGATCTCCCACTGGCCCTACTTGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCCTACAACCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTCACTGCCCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT
GTGTGCCGGGCGGATGGCGACCCGCCGCCCGCCATCCTCTGGCTCTACCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGCCAACGCGGGCGGCAACGAC
TCCATGCCCGCCACCTGCATGTGCGCAGCTACTCGCCGACTGGCCCCATCAGCCCAACA
GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCCTTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTCGTCTCTCTTGCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGGCGGGGGGCAGGGACCCCCG
GGCGGCCGGGCAGGGGAAGGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCCCTTCCACCTC
CTCCCTACCCTTCTACACACGTTCTCTTTCTCCCTCCCGCCTCCGTCCCTGCTGCCCCCG
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT
TATGAAAACCTTGAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFFNNLFLNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSSIPTEALSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGNLETILDSNPLA
CDCRLLWVFRRRWRLNFNRRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIAILWLSPRKHLVSAKSNGRLLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDSPAHHLHVRSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGN TKH NIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

090273079220550

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCCGGGGATTGAGGCTCGCCAGCGCCCAGCC
AGGGAGCCGGCCGGGAAGCGCGAATGGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTTGCGCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTG
CTCATCATGCTCATCTTCCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCCACTTCCTGC
GCCCCCAGGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGGAAATGGGGAGGGAGGGCGGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCCTGCTGCTCTGCATTTGGGTTATTATTATTTTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACA
AACAAAAACA

FIGURE 32

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDET VVAGGT VVLKCQVKDHEDSSLQW
SNPAQQTL YFGEKRALRDNRIQLVTSTPHELSSISISNVALADEGEYTC SIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRI QEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQR IEVLYTPTAMIRPDPPHPREGQ
KLL LHCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMG SYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLT HEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	Male	100	0	100
Marital Status	Married	75	0	100
Education	High School	15	0	100
Occupation	Manager	45	0	100
Income	\$50,000	20,000	0	100,000
Health Status	Good	85	0	100
Exercise Frequency	Weekly	60	0	100
Stress Level	Low	30	0	100
Sleep Quality	Good	70	0	100
Dietary Habits	Healthy	55	0	100
Alcohol Consumption	Low	20	0	100
Tobacco Use	Never	90	0	100
Family Size	2	1	0	5
Home Ownership	Owned	80	0	100
Commute Time	30 min	15 min	0	60 min
Work-Life Balance	Good	65	0	100
Job Satisfaction	High	75	0	100
Leadership Skills	Strong	80	0	100
Teamwork Ability	Excellent	85	0	100
Communication Skills	Good	70	0	100
Problem Solving	Strong	75	0	100
Adaptability	High	80	0	100
Resilience	Good	70	0	100
Emotional Stability	High	85	0	100
Self-Motivation	Strong	80	0	100
Time Management	Good	75	0	100
Decision Making	Strong	80	0	100
Conflict Resolution	Good	70	0	100
Networking Skills	Strong	85	0	100
Public Speaking	Good	75	0	100
Writing Skills	Strong	80	0	100
Technical Skills	Good	70	0	100
Language Proficiency	High	85	0	100
Cultural Awareness	Strong	80	0	100
Global Perspective	Good	75	0	100
Interpersonal Skills	Strong	85	0	100
Empathy	Good	70	0	100
Active Listening	Strong	80	0	100
Collaboration	Good	75	0	100
Leadership Potential	High	85	0	100
Team Player	Strong	80	0	100
Initiative	Good	70	0	100
Proactivity	Strong	85	0	100
Accountability	Good	75	0	100
Responsibility	Strong	80	0	100
Organizational Skills	Good	70	0	100
Attention to Detail	Strong	85	0	100
Time Management Skills	Good	75	0	100
Task Completion	Strong	80	0	100
Efficiency	Good	70	0	100
Productivity	Strong	85	0	100
Quality Work	Good	75	0	100
Consistency	Strong	80	0	100
Reliability	Good	70	0	100
Dependability	Strong	85	0	100
Trustworthiness	Good	75	0	100
Integrity	Strong	80	0	100
Honesty	Good	70	0	100
Openness	Strong	85	0	100
Transparency	Good	75	0	100
Communication Skills	Strong	80	0	100
Active Listening	Good	70	0	100
Public Speaking	Strong	85	0	100
Writing Skills	Good	75	0	100
Technical Skills	Strong	80	0	100
Language Proficiency	Good	70	0	100
Cultural Awareness	Strong	85	0	100
Global Perspective	Good	75	0	100
Interpersonal Skills	Strong	80	0	100
Empathy	Good	70	0	100
Active Listening	Strong	85	0	100
Collaboration	Good	75	0	100
Leadership Potential	Strong	80	0	100
Team Player	Good	70	0	100
Initiative	Strong	85	0	100
Proactivity	Good	75	0	100
Accountability	Strong	80	0	100
Responsibility	Good	70	0	100
Organizational Skills	Strong	85	0	100
Attention to Detail	Good	75	0	100
Time Management Skills	Strong	80	0	100
Task Completion	Good	70	0	100
Efficiency	Strong	85	0	100
Productivity	Good	75	0	100
Quality Work	Strong	80	0	100
Consistency	Good	70	0	

GGGGGTTAGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTTCTCCTTTCTGCTG
CTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTTTACCATTATTTCTGCATGGCAATTC
CCTCACTCGACTTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATG
AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTTTCTGGGGCTGCAGCTGGTGAAAAG
CTGCACATCAACAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAAATTTATTACGAGATATAGACCCGGGGGCTTCCAG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAACACATTCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACCGAGGTACAAAGATCCAGGCAACTGCGAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCAGGGTTCGGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT
TAGAAAGGATTTTATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTGCGGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
GTTTGTCACTCCGCCTTACCCTGGTGGGCATGCTCGTGTTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAAATCCCTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTAACCAATCCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTCGCACAAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTTGAAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAAGCCCAGCACGACCTGCTGGAAG
AACTGACAGTGCCTTCGCCCTCGGCCCGGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACTTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLRLDIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPEYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSRPCPGGCSCDHIPGSGMKMNCNNRNVSSLADLKP
KLSNVQELFLRDNKHHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLDDLRLWLYMDSNY
LDTLSREKFAGLQNLLEYLNVEYNAIQILILPGTFNAMPKLRILILNNNLLRSLPVDVVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSCCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFVTSFTVVGMLVFILNRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, .
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

200720"0922050

[illegible]

AGTCGACTGCGTCCCCTGTATACCGGCGCCAGCTGTGTTCTTGACCCCAAGAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTTCGCGGCCTAAGGGAACTGTTGGC
CGCTGGGCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTTCGGGAGCGAGGGCGAGGGG
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTTCGGGGCCTCAG
AGAATGAGGCCGGCGTTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCCGGGCGG
CGGCGAACACCCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTTCGTTCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG
GCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTTCGACTGGAGCGCAGGCGTTCCCACT
GCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCCTCCGACCCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTTGAAGTCTTGTTGTCTGCGCCGCGCCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCAGAGTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGGAAGGACGGCCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGGGTGCCACCAGGCGCCCGCGCCACT
GCAACCAGCCCCGTGCCGACAGAAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
ACCATTGTCCCTGAACAAGACAATTGTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCCGGGCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCTTGCTGGCGGAGTCCCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTAC
TTGTGTAAC TGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGAGAA
TTTGAGAAAGTGATTGAACTTTTCAAGACATTGGAACAAATAGAACACAATATAATTTACA
TTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAGGCTAGGAGTAT
ATTGTTTCGAAATCCCAGGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPI SVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 36

FIGURE 37

CGGACGCGTGGGATTTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGCGCGCCCGCGGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCGCGCGTGGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTTCACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTTCATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA
AACTGCCTACAATAACAGAACAGCCTGTCACCACCACATTCCCTGTAACCACGGGTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTTCAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TAACAGTGAACGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT
TCTCAGTAGAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCCTGCTGTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT
GTTATTTGTTTCACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTCTA
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAAAAAAAAA

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FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFCTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLACTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

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FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCCCACGGCGCCCGCGGGCTGGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGGCCCTCCTGC
CTTCCCTGTCCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCCCTGTGCCCGATGCTCAGGACCTGAGGAATCAAACGTGTTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTACCACATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGAAAGTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGSGHCDQCAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFG
IIICALATLAAKGD LVFTAIFIGAVAAMTGYWLSERSDRVLEGF I KGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCCGCTGGCGTCCGGCGCCCCACAAGCTGGTCCGCTTTGCCTCGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTGAGGGTACCAGGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTTCTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCAATTGTTTACTTGTCTGTAC
TGGATCTGGGCTAAAGTCCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT
AAAA

CIVIL ENGINEERING	
2071	70
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2216	70
2217	70
2218	70
2219	70
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2224	70
2225	70
2226	70
2227	70
2228	70
2229	70
2230	70
2231	70
2232	70
2233	

Signal sequence:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

[illegible]

GTCTGTTCCCAAGGAGTCCCTTCGGCGGGCTGTTGTGTACGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCTCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGT CATCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT
CTTGTTTTTTGGCATCTGGTTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTCTGGTGTTGAGCCTGGTGGCTCACCGCCTATCATCTGCATTGTCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCTACCACTGCTGAGTGGCCTGGAAC TTGTTTAAA
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGCAGGAATCTGCACTCAACTGCCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTTCCTTGTTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGCGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	2.5	9	16
Income	15.5	5.5	10	25
Health status	0.5	0.5	0	1
Employment status	0.5	0.5	0	1
Home ownership	0.5	0.5	0	1
Vehicle ownership	0.5	0.5	0	1
Life satisfaction	4.5	1.5	1	7
Health satisfaction	4.5	1.5	1	7
Financial satisfaction	4.5	1.5	1	7
Relationship satisfaction	4.5	1.5	1	7
Community satisfaction	4.5	1.5	1	7
Environment satisfaction	4.5	1.5	1	7
Security satisfaction	4.5	1.5	1	7
Quality of life	4.5	1.5	1	7
Life expectancy	75	5	60	90
Health expectancy	65	5	50	80
Financial expectancy	65	5	50	80
Relationship expectancy	65	5	50	80
Community expectancy	65	5	50	80
Environment expectancy	65	5	50	80
Security expectancy	65	5	50	80
Quality of life expectancy	65	5	50	80

Signal sequence:

Transmembrane domain:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

[illegible]

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCCGCAGGCCCCAGCTCAG
GCTCGTGCCCAACCACCAAGTTCCAGTGCCGCACCAGTGCGCTTATGCGTGCCCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCCAACGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCCTCTGTCGGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCAGGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDCSDGSDEEEECRIEPCCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

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FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGGCACAGATGCGG
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCTAGGCTGGATCCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTGATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTTCAATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGTCT
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTCT
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTC AAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGGACACGGA
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCCACTGGGT
GTTGTTCCCTAAGAACTGATTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCTTTCTTCTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAA

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FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPFGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

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FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGAATGATGGCAGCATAT
CACAATTTAGGAACTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA
CCGGTGCAACATGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACCTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAACACCTCTGTTTTCTTGCTCTATACAG
CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAA

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FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD F WIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLLV
VTTVVCWVWICRKRKREQPD PSTKKQHTIWPSPHQGN SPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

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FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTTCAGCATGCGCTTGTGGACCCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAATC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCTGTTCCACTAACATTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAACTCTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGTACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTTATACAATG

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APPENDIX 1	
List of variables	
Age	1
Gender	2
Marital status	3
Education	4
Occupation	5
Income	6
Health status	7
Family size	8
Religion	9
Political affiliation	10
Home ownership	11
Auto ownership	12
Life insurance	13
Retirement savings	14
Charitable contributions	15
Volunteer work	16
Travel frequency	17
Exercise frequency	18
Alcohol consumption	19
Tobacco use	20
Stress level	21
Life satisfaction	22
Overall health	23
Family income	24
Family size	25
Family structure	26
Family stability	27
Family cohesion	28
Family communication	29
Family conflict	30
Family support	31
Family resources	32
Family strengths	33
Family weaknesses	34
Family challenges	35
Family opportunities	36
Family goals	37
Family values	38
Family beliefs	39
Family attitudes	40
Family behaviors	41
Family emotions	42
Family thoughts	43
Family feelings	44
Family actions	45
Family reactions	46
Family responses	47
Family outcomes	48
Family impacts	49
Family effects	50
Family consequences	51
Family results	52
Family achievements	53
Family successes	54
Family failures	55
Family lessons	56
Family wisdom	57
Family knowledge	58
Family skills	59
Family abilities	60
Family talents	61
Family gifts	62
Family blessings	63
Family curses	64
Family prayers	65
Family hopes	66
Family dreams	67
Family wishes	68
Family desires	69
Family needs	70
Family wants	71
Family requirements	72
Family necessities	73
Family comforts	74
Family pleasures	75
Family joys	76
Family happiness	77
Family well-being	78
Family health	79
Family wealth	80
Family power	81
Family influence	82
Family reputation	83
Family status	84
Family honor	85
Family respect	86
Family dignity	87
Family pride	88
Family shame	89
Family guilt	90
Family sin	91
Family righteousness	92
Family holiness	93
Family purity	94
Family integrity	95
Family honesty	96
Family truthfulness	97
Family faithfulness	98
Family loyalty	99
Family obedience	100

Signal sequence:

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCAGAGAGCTCTTTCTCCCCA
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACCTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTTCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTTGTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAA

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FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGWVGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

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FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTCTGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTAC

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FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLQLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISIIQKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTCTAA
GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAAC TGATTTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTTTGAGGCTTTGGCAGTCTTCATTTACTACCCTTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTTATTAATAAATTTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

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FIGURE 58

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKGKLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKPNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

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FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCTGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGA
AGAGTTATGCCGGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTACAAGTAACATGA
CCTTGCGTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCCTAATTGAGTTTTTCCAGATATTTCTGAATATAAAAAATA
ATGACTTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAAGTGGTTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATATAGTTGAAAAGTACTTGCGAGA
AGATACAGTACAGTCAAGTAAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGGAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAGAGAACAT
CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGTCTTGAATAGGAAGTTTTTAATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
TAGTTTTGGGGAAAAGATTCTCAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
AAAATATTATATATAAAAGTAAAAA

090236"0707

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	Male	Female		
Marital Status	Married	Single		
Education	High School	College		
Income	\$15,000	\$25,000		
Health Status	Good	Fair		
Exercise Frequency	Weekly	Monthly		
Stress Level	Low	High		
Sleep Quality	Good	Poor		
Dietary Habits	Healthy	Unhealthy		
Alcohol Consumption	None	Occasional		
Tobacco Use	Non-smoker	Smoker		
Family History	No	Yes		
Current Medication	No	Yes		
Chronic Conditions	No	Yes		
Work Satisfaction	High	Low		
Life Satisfaction	High	Low		
Overall Health Score	75	15	50	100

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

Serine carboxypeptidases, serine active site.

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT
TTTTCCCTTTCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATCGGGACCCTGGGTCT
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTTTGGTCTGACCACTCTGCCTTGTGTTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCA
GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT
CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTTCTTGGGGAACAAAGGTGAATGGGGAGGTAAGAAGGGGTAAATTTTGTG
ACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACCTTTAAGAAAAAATTTAAGAAGGTACATCTGCAAAAGCAAA

090273-0400

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	Male	100%		
Marital Status	Married	100%		
Education	High School	100%		
Occupation	Teacher	100%		
Income	\$15,000	\$5,000	\$10,000	\$20,000
Health Status	Good	100%		
Smoking Status	Non-smoker	100%		
Alcohol Consumption	None	100%		
Exercise Frequency	Weekly	100%		
Stress Level	Low	100%		
Sleep Quality	Good	100%		
Dietary Habits	Healthy	100%		
Family Size	2	1	1	3
Home Ownership	Owned	100%		
Vehicle Ownership	Owned	100%		
Insurance Coverage	Health	100%		
Religious Beliefs	Christian	100%		
Political Views	Conservative	100%		
Travel Frequency	Monthly	100%		
Pet Ownership	Dog	100%		
Gardening Interest	High	100%		
Volunteering	Yes	100%		
Charitable Contributions	\$500	\$200	\$0	\$1,000
Community Involvement	Active	100%		
Neighborhood Satisfaction	High	100%		
Local Government Trust	High	100%		
Environmental Awareness	High	100%		
Waste Recycling Rate	80%	10%	70%	90%
Water Conservation Practices	Yes	100%		
Renewable Energy Usage	Yes	100%		
Local Food Consumption	Yes	100%		
Organic Food Purchase	Yes	100%		
Local Market Visitation	Weekly	100%		
Community Garden Participation	Yes	100%		
Local Festival Attendance	Yes	100%		
Neighborhood Watch Participation	Yes	100%		
Local Business Patronage	Yes	100%		
Community Meeting Attendance	Yes	100%		
Local Issue Advocacy	Yes	100%		
Neighborhood Improvement Projects	Yes	100%		
Local History Interest	High	100%		
Local Landmark Preservation	Yes	100%		
Local Art and Culture Support	Yes	100%		
Local Music Scene Engagement	Yes	100%		
Local Theater Attendance	Yes	100%		
Local Film Festival Participation	Yes	100%		
Local Sports Team Support	Yes	100%		
Local Event Organization	Yes	100%		
Local Volunteer Work	Yes	100%		
Local Charity Support	Yes	100%		
Local Business Association Membership	Yes	100%		
Local Chamber of Commerce Membership	Yes	100%		
Local Historical Society Membership	Yes	100%		
Local Garden Club Membership	Yes	100%		
Local Book Club Membership	Yes	100%		
Local Film Society Membership	Yes	100%		
Local Music Society Membership	Yes	100%		
Local Theater Group Membership	Yes	100%		
Local Sports Team Membership	Yes	100%		
Local Event Committee Membership	Yes	100%		
Local Volunteer Group Membership	Yes	100%		
Local Charity Board Membership	Yes	100%		
Local Business Board Membership	Yes	100%		
Local Chamber of Commerce Board Membership	Yes	100%		
Local Historical Society Board Membership	Yes	100%		
Local Garden Club Board Membership	Yes	100%		
Local Book Club Board Membership	Yes	100%		
Local Film Society Board Membership	Yes	100%		
Local Music Society Board Membership	Yes	100%		
Local Theater Group Board Membership	Yes	100%		
Local Sports Team Board Membership	Yes	100%		
Local Event Committee Board Membership	Yes	100%		
Local Volunteer Group Board Membership	Yes	100%		
Local Charity Board Board Membership	Yes	100%		
Local Business Board Board Membership	Yes	100%		
Local Chamber of Commerce Board Board Membership	Yes	100%		
Local Historical Society Board Board Membership	Yes	100%		
Local Garden Club Board Board Membership	Yes	100%		
Local Book Club Board Board Membership	Yes	100%		
Local Film Society Board Board Membership	Yes	100%		
Local Music Society Board Board Membership	Yes	100%		
Local Theater Group Board Board Membership	Yes	100%		
Local Sports Team Board Board Membership	Yes	100%		
Local Event Committee Board Board Membership	Yes	100%		
Local Volunteer Group Board Board Membership	Yes	100%		
Local Charity Board Board Board Membership	Yes	100%		
Local Business Board Board Board Membership	Yes	100%		
Local Chamber of Commerce Board Board Board Membership	Yes	100%		
Local Historical Society Board Board Board Membership	Yes	100%		
Local Garden Club Board Board Board Membership	Yes	100%		
Local Book Club Board Board Board Membership	Yes	100%		
Local Film Society Board Board Board Membership	Yes	100%</		

Signal sequence:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

Variable	Mean	SD	Min	Max
Age	38.5	12.5	18	65
Gender	0.5	0.5	0	1
Marital status	0.7	0.5	0	1
Education	12.5	2.5	8	16
Income	3500	1500	1000	8000
Health status	0.8	0.4	0	1
Stress level	4.5	1.5	1	7
Life satisfaction	5.5	1.5	1	9
Work-life balance	6.5	1.5	1	9
Family support	7.5	1.5	1	9
Community support	6.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Quality of life	7.5	1.5	1	9
Overall well-being	6.5	1.5	1	9
Life expectancy	75	5	60	90
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5	1.5	1	9
Healthcare costs	1500	500	500	3000
Health insurance	0.9	0.1	0	1
Healthcare quality	8.5	1.5	1	9
Healthcare access	8.5			

Signal sequence:

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315, 320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

09002736 "071001

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGCGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA
GGCAGACACTCGGTTCGTTCTAGTGGATAGGGGTCATGACCGGTTTCTCCTAGACGGGGCCC
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTTCGGGTACCGCGGGTGCTTTGGGCCGAC
CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGCTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCCTC
AGATCCAGACTTCCTTGCCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTGAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAATCTTTACCCTGCTT
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCCAACCTAAGCTTTTGTCTCTTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTTGGGACCTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCC
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
GAACCTATATGACCCATACCATTTTGTAGCCAACACCATTTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAG
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCTCTACGTGCCAAGATTCCCTGCTGTTTCCTAGGGGAGCCCTCAACAAAATTA
CATTGCTGGAAC TAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCTATC
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCCTTTCAGCTGATACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGGCGTG
ATGGTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GCACTCCATCTCAAAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSGDFTFLYL
PGWTKGQVWINGFNLGRYWTKQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTCAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAACTCAGGCAGCACATTTACGCAACGCCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCAGAAGCTAAAATTCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCTTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTTCATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAACGACT
GACTTGTTTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTTG
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTTGCAAATGGGATTTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTTAAGTCATTTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTAAATTGTTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAAAAA

090270-0100

FIGURE 68

MAYMLKKLLISYISIIICVYGFICLYTLFWLFRIPPLKEYSF EKVREESSFSDIPDVKNDF AFL
LHMVDQYDQLYSKRFGVFLSEVSENKLREISLNHEWTFEKL RQHISRNAQDKQELHLFMLS G
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLES LRELRLHLKILHVKS NLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNC ELERIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKN LESLYFSNNKLES LPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPK QLFKCIKLRTLNLGQNCITSLP
EKVGQLS QLTQLELKGNC LDR LPAQLGQCRMLKKSGLVVEDH LFD TLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACGCGTCCGGCCCTTCTCTCTGGACTTTGCATTTCCATTCTTTTTCATTGACAAACTGACTTTTTTTTATTTCT
TTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT
CTGTGTTTTGGGGTTTCTTCTTCCCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCAGTGG
GCTCAGTGTCTTGTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGGTATCCTGGCGGCCCTTGCTCCTGCTGATAGTTGTCTGTCTGTCTTTACTTCAAATACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAAACCAGACAAGGTGTGGTGGGCCAAG
AACAGCCAGGCCAAAACCATTGCCACGGAGTCTTGTCTCTGCCCTGCAGTGTGTGAAGGATATAGAATGTGTGCC
AGTTTTGATTCCCTGCCACCTTGCTGTGTGCGACATAAATGAGGCCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGGCAACCCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACAGTCA
CACAGCTGCTCTATTTCTACACAAATCTACCCCTTGCGTGGCTGGAAGTACGTTTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTCCGTCTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA
AGAAGGCTCATGCCATTGACCCTCTTAATTCTCTCTCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAAAAACATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCTTAACATCTCTATTCCAACTGT
GGCGGTTACCTGGATACCTTGAAGGATCCTTACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTTCAAAGAGATTTTCTAGAAATAGAC
AAACAGTGCAAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCCACCTTGAATCGTCATCAAACCTCTCTGACTGTCTGTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTTTCTGCTTCTTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA
GACCCAACTTGCAGACCAAAATTATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCCTGGGCAAATATAACACCAGCATGGCTCTTTTTGAATCCAATTCA
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACCTCTTTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTTGGTGGTGTCTTGTATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAGGTGTATCCCTTATTTGGACACTATGGGAGA
TTCCAGTTTAATGCCTTTAAATTTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTTGATATGTGAT
AGCAGTGACCACCAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG
AAAACAGATTCATCATAGGACCCATTTCGTCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTTCAGCAT
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTTCTTCATGGTTCTAGCTCTG
AATGTGGTGAATGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	1.2	0.4	1	2
Marital status	1.5	0.5	1	3
Education	12.8	2.1	9	16
Income	15.5	3.2	10	25
Occupation	1.8	0.6	1	3
Health status	1.2	0.4	1	2
Stress level	2.5	1.2	1	5
Life satisfaction	3.8	1.5	1	6
Resilience	4.2	1.8	1	7
Optimism	4.5	2.0	1	7
Gratitude	4.8	2.2	1	7
Forgiveness	5.1	2.5	1	7
Empathy	5.4	2.8	1	7
Compassion	5.7	3.0	1	7
Kindness	6.0	3.2	1	7
Generosity	6.3	3.5	1	7
Patience	6.6	3.8	1	7
Self-control	6.9	4.0	1	7
Perseverance	7.2	4.2	1	7
Determination	7.5	4.5	1	7
Confidence	7.8	4.8	1	7
Trust	8.1	5.0	1	7
Hope	8.4	5.2	1	7
Love	8.7	5.5	1	7
Peace	9.0	5.8	1	7
Harmony	9.3	6.0	1	7
Balance	9.6	6.2	1	7
Stability	9.9	6.5	1	7
Consistency	10.2	6.8	1	7
Reliability	10.5	7.0	1	7
Integrity	10.8	7.2	1	7
Honesty	11.1	7.5	1	7
Truthfulness	11.4	7.8	1	7
Openness	11.7	8.0	1	7
Transparency	12.0	8.2	1	7
Accountability	12.3	8.5	1	7
Responsibility	12.6	8.8	1	7
Commitment	12.9	9.0	1	7
Dedication	13.2	9.2	1	7
Devotion	13.5	9.5	1	7
Zeal	13.8	9.8	1	7
Enthusiasm	14.1	10.0	1	7
Passion	14.4	10.2	1	7
Energy	14.7	10.5	1	7
Vitality	15.0	10.8	1	7
Strength	15.3	11.0	1	7
Power	15.6	11.2	1	7
Influence	15.9	11.5	1	7
Impact	16.2	11.8	1	7
Legacy	16.5	12.0	1	7
Contribution	16.8	12.2	1	7
Service	17.1	12.5	1	7
Helpfulness	17.4	12.8	1	7
Usefulness	17.7	13.0	1	7
Value	18.0	13.2	1	7
Importance	18.3	13.5	1	7
Significance	18.6	13.8	1	7
Meaning	18.9	14.0	1	7
Purpose	19.2	14.2	1	7
Goal	19.5	14.5	1	7
Direction	19.8	14.8	1	7
Focus	20.1	15.0	1	7
Attention	20.4	15.2	1	7
Interest	20.7	15.5	1	7
Curiosity	21.0	15.8	1	7
Wonder	21.3	16.0	1	7
Awe	21.6	16.2	1	7
Reverence	21.9	16.5	1	7
Respect	22.2	16.8	1	7
Honor	22.5	17.0	1	7
Dignity	22.8	17.2	1	7
Grace	23.1	17.5	1	7
Beauty	23.4	17.8	1	7
Art	23.7	18.0	1	7
Music	24.0	18.2	1	7
Dance	24.3	18.5	1	7
Performance	24.6	18.8	1	7
Entertainment	24.9	19.0	1	7
Fun	25.2	19.2	1	7
Play	25.5	19.5	1	7
Recreation	25.8	19.8	1	7
Leisure	26.1	20.0	1	7
Relaxation	26.4	20.2	1	7
Rest				

Signal sequence:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	Male	10	0	20
Marital status	Married	15	0	30
Education	High school	5	0	10
Occupation	Unemployed	10	0	20
Income	Low	15	0	30
Health status	Good	10	0	20
Smoking	Non-smoker	15	0	30
Alcohol	Non-drinker	10	0	20
Exercise	Regular	5	0	10
Stress	Low	10	0	20
Sleep	Good	15	0	30
Diet	Healthy	10	0	20
Family size	Small	5	0	10
Religion	Christian	10	0	20
Politics	Conservative	15	0	30
Travel	Domestic	10	0	20
Shopping	Online	5	0	10
Reading	Frequent	10	0	20
Writing	Regular	5	0	10
Art	Interested	10	0	20
Music	Enthusiast	15	0	30
Gardening	Regular	5	0	10
Cooking	Enthusiast	10	0	20
Volunteering	Regular	5	0	10
Charitable	Interested	10	0	20
Philosophy	Interested	10	0	20
Science	Interested	10	0	20
History	Interested	10	0	20
Geography	Interested	10	0	20
Language	Interested	10	0	20
Mathematics	Interested	10	0	20
Physics	Interested	10	0	20
Chemistry	Interested	10	0	20
Biology	Interested	10	0	20
Medicine	Interested	10	0	20
Law	Interested	10	0	20
Business	Interested	10	0	20
Economics	Interested	10	0	20
Psychology	Interested	10	0	20
Sociology	Interested	10	0	20
Anthropology	Interested	10	0	20
Archaeology	Interested	10	0	20
Art History	Interested	10	0	20
Music History	Interested	10	0	20
Literature	Interested	10	0	20
Classical Music	Interested	10	0	20
Modern Music	Interested	10	0	20
Traditional Music	Interested	10	0	20
World Music	Interested	10	0	20
Classical Art	Interested	10	0	20
Modern Art	Interested	10	0	20
Traditional Art	Interested	10	0	20
World Art	Interested	10	0	20
Classical Literature	Interested	10	0	20
Modern Literature	Interested	10	0	20
Traditional Literature	Interested	10	0	20
World Literature	Interested	10	0	20
Classical Music History	Interested	10	0	20
Modern Music History	Interested	10	0	20
Traditional Music History	Interested	10	0	20
World Music History	Interested	10	0	20
Classical Art History	Interested	10	0	20
Modern Art History	Interested	10	0	20
Traditional Art History	Interested	10	0	20
World Art History	Interested	10	0	20
Classical Literature History	Interested	10	0	20
Modern Literature History	Interested	10	0	20
Traditional Literature History	Interested	10	0	20
World Literature History	Interested	10	0	20
Classical Music History	Interested	10	0	20
Modern Music History	Interested	10	0	20
Traditional Music History	Interested	10	0	20
World Music History	Interested	10	0	20
Classical Art History	Interested	10	0	20
Modern Art History	Interested	10	0	20
Traditional Art History	Interested	10	0	20
World Art History	Interested	10	0	20
Classical Literature History	Interested	10	0	20
Modern Literature History	Interested	10	0	20
Traditional Literature History	Interested	10	0	20
World Literature History	Interested	10	0	20

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	Male	10	0	20
Marital status	Married	15	0	30
Education	High school	5	0	10
Occupation	Unemployed	10	0	20
Income	Low	15	0	30
Health status	Good	10	0	20
Smoking	Non-smoker	15	0	30
Alcohol	Non-drinker	10	0	20
Exercise	Regular	5	0	10
Stress	Low	10	0	20
Sleep	Good	15	0	30
Diet	Healthy	10	0	20
Family size	Small	5	0	10
Religion	Christian	10	0	20
Politics	Conservative	15	0	30
Travel	Domestic	10	0	20
Shopping	Online	5	0	10
Reading	Frequent	10	0	20
Writing	Regular	5	0	10
Art	Interested	10	0	20
Music	Enthusiast	15	0	30
Gardening	Regular	5	0	10
Cooking	Enthusiast	10	0	20
Volunteering	Regular	5	0	10
Charitable	Interested	10	0	20
Philosophy	Interested	10	0	20
Science	Interested	10	0	20
History	Interested	10	0	20
Geography	Interested	10	0	20
Language	Interested	10	0	20
Mathematics	Interested	10	0	20
Physics	Interested	10	0	20
Chemistry	Interested	10	0	20
Biology	Interested	10	0	20
Medicine	Interested	10	0	20
Law	Interested	10	0	20
Business	Interested	10	0	20
Economics	Interested	10	0	20
Psychology	Interested	10	0	20
Sociology	Interested	10	0	20
Anthropology	Interested	10	0	20
Archaeology	Interested	10	0	20
Art History	Interested	10	0	20
Music History	Interested	10	0	20
Literature	Interested	10	0	20
Classical Music	Interested	10	0	20
Modern Music	Interested	10	0	20
Traditional Music	Interested	10	0	20
World Music	Interested	10	0	20
Classical Art	Interested	10	0	20
Modern Art	Interested	10	0	20
Traditional Art	Interested	10	0	20
World Art	Interested	10	0	20
Classical Literature	Interested	10	0	20
Modern Literature	Interested	10	0	20
Traditional Literature	Interested	10	0	20
World Literature	Interested	10	0	20
Classical Music History	Interested	10	0	20
Modern Music History	Interested	10	0	20
Traditional Music History	Interested	10	0	20
World Music History	Interested	10	0	20
Classical Art History	Interested	10	0	20
Modern Art History	Interested	10	0	20
Traditional Art History	Interested	10	0	20
World Art History	Interested	10	0	20
Classical Literature History	Interested	10	0	20
Modern Literature History	Interested	10	0	20
Traditional Literature History	Interested	10	0	20
World Literature History	Interested	10	0	20
Classical Music History	Interested	10	0	20
Modern Music History	Interested	10	0	20
Traditional Music History	Interested	10	0	20
World Music History	Interested	10	0	20
Classical Art History	Interested	10	0	20
Modern Art History	Interested	10	0	20
Traditional Art History	Interested	10	0	20
World Art History	Interested	10	0	20
Classical Literature History	Interested	10	0	20
Modern Literature History	Interested	10	0	20
Traditional Literature History	Interested	10	0	20
World Literature History	Interested	10	0	20

FIGURE 72

MRPQELPRLAFPLLLLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEFWWYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEFW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 72

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGC
AGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA
TGGATTCTGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAACAGAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTGATTTGTGTACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC
TATGTCAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA
AACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCTAATAATATCCCCTGGGAGAAAGGAGTTTTGCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGAC
CCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTA
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTCTGAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTTCA
GTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTTTATTTTTGCTGAGACTAATCTT
ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG
TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA
AGCATTTAGAAAACCTT

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FIGURE 74

MARCFSLVLLLTISIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIVKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTTCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAA
ACTGCCGCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCCGCTTGGATATTTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAACGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC
AGCTATTCAAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCCTTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTTCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCAC
TAACCCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCCGTAATAAAAAGATTGGGATT
TCCTTTTG

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FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

0902760001

Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	Male	10.5	0	20
Marital status	Married	15.2	0	20
Education	High school	12.8	0	20
Occupation	Unemployed	18.5	0	20
Income	Low	15.3	0	20
Health status	Good	12.1	0	20
Smoking status	Non-smoker	10.8	0	20
Alcohol consumption	None	11.5	0	20
Exercise frequency	Low	13.2	0	20
Stress level	High	16.7	0	20
Sleep quality	Poor	14.9	0	20
Appetite	Normal	11.0	0	20
Weight change	Stable	12.5	0	20
Blood pressure	Normal	13.8	0	20
Blood sugar	Normal	14.2	0	20
Cholesterol	Normal	15.1	0	20
Heart rate	Normal	16.0	0	20
Respiratory rate	Normal	17.5	0	20
Oxygen saturation	Normal	18.2	0	20
Temperature	Normal	19.0	0	20
Pulse rate	Normal	19.8	0	20
Respiratory rate	Normal	20.5	0	20
Oxygen saturation	Normal	21.2	0	20
Temperature	Normal	22.0	0	20
Pulse rate	Normal	22.8	0	20
Respiratory rate	Normal	23.5	0	20
Oxygen saturation	Normal	24.2	0	20
Temperature	Normal	25.0	0	20
Pulse rate	Normal	25.8	0	20
Respiratory rate	Normal	26.5	0	20
Oxygen saturation	Normal	27.2	0	20
Temperature	Normal	28.0	0	20
Pulse rate	Normal	28.8	0	20
Respiratory rate	Normal	29.5	0	20
Oxygen saturation	Normal	30.2	0	20
Temperature	Normal	31.0	0	20
Pulse rate	Normal	31.8	0	20
Respiratory rate	Normal	32.5	0	20
Oxygen saturation	Normal	33.2	0	20
Temperature	Normal	34.0	0	20
Pulse rate	Normal	34.8	0	20
Respiratory rate	Normal	35.5	0	20
Oxygen saturation	Normal	36.2	0	20
Temperature	Normal	37.0	0	20
Pulse rate	Normal	37.8	0	20
Respiratory rate	Normal	38.5	0	20
Oxygen saturation	Normal	39.2	0	20
Temperature	Normal	40.0	0	20
Pulse rate	Normal	40.8	0	20
Respiratory rate	Normal	41.5	0	20
Oxygen saturation	Normal	42.2	0	20
Temperature	Normal	43.0	0	20
Pulse rate	Normal	43.8	0	20
Respiratory rate	Normal	44.5	0	20
Oxygen saturation	Normal	45.2	0	20
Temperature	Normal	46.0	0	20
Pulse rate	Normal	46.8	0	20
Respiratory rate	Normal	47.5	0	20
Oxygen saturation	Normal	48.2	0	20
Temperature	Normal	49.0	0	20
Pulse rate	Normal	49.8	0	20
Respiratory rate	Normal	50.5	0	20
Oxygen saturation	Normal	51.2	0	20
Temperature	Normal	52.0	0	20
Pulse rate	Normal	52.8	0	20
Respiratory rate	Normal	53.5	0	20
Oxygen saturation	Normal	54.2	0	20
Temperature	Normal	55.0	0	20
Pulse rate	Normal	55.8	0	20
Respiratory rate	Normal	56.5	0	20
Oxygen saturation	Normal	57.2	0	20
Temperature	Normal	58.0	0	20
Pulse rate	Normal	58.8	0	20
Respiratory rate	Normal	59.5	0	20
Oxygen saturation	Normal	60.2	0	20
Temperature	Normal	61.0	0	20
Pulse rate	Normal	61.8	0	20
Respiratory rate	Normal	62.5	0	20
Oxygen saturation	Normal	63.2	0	20
Temperature	Normal	64.0	0	20
Pulse rate	Normal	64.8	0	20
Respiratory rate	Normal	65.5	0	20
Oxygen saturation	Normal	66.2	0	20
Temperature	Normal	67.0	0	20
Pulse rate	Normal</			

[illegible]

FIGURE 78

MGLLLLVLPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPPVHHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

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"00720" 9E2056D

[illegible]

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCCAG
CCTGTCTGTCTGTCGTTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTGCACACCGATCCTG
GGCTTCGCTCGATTTGCCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
CGGGTCGTCTGTGTCTCTCTCCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCAGGGGCTCT
GAGGAGGTGACGCGCGGGGCTCCCGCACCCCTGGCCTTGCCCGCATTCTCCCTCTCTCCCAG
GTGTGAGCAGCCTATCAGTCACCAATGTCCGCAGCCTGGATCCCCGGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
TTTTACCAGAGGCTTGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAATAATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTTCTTTACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAATGG
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
GCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA
GAAGGACCACATGTGGGCCTTGTTCAAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA
AAACTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCTCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAA
CTTCTAGTAATTGTACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCACAAGAGAGTTTACAGGATT
AGAACCAATTGTTTCTGATGTCTATCAGAGGCATTGTAGAGATTTCTTAGAATCCAGCAAT
AATGGTAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT
CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAATATTAAGTATGTCAAC
AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT
ACTTTGTTAAAAAACTGCTGAGGCTTCATAATCATGGCTCTTAGAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEF SVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVT FVDKAVCRNNGFFSYHMPNWF GTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAF FTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

090226 072056

[illegible][illegible]

FIGURE 84

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSY PQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQQRMLCTRDSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

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FIGURE 85

AAGGAGGCTGGGAGGAAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAAATTTAGCCCATCCACTCTCTTCCCTCCCAAACACACATGTGCATGTACACACACATACA
CACACATACACCTTCTCTCTCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC
TAAAGCCTTAAGGACAGGCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG
CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTGAGGAG
TTCGAGACCAGCTGGCCAAACATGGAGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC
AGGTGCCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGT
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACCTCTGCATCCTCTTCTTCCAGGGCTGCCCCCTGATGGGGCCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCCCG
GTGTAGAAATGACTGCCCTGGGAGGGTGGTTCCTTGGGCCCTGGCAGGGTGTCTGACCCTTACCCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCGTGGTACCCTGGCATGTTCCCTGCCCCCTCA
GTGTGCCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCTTACC CGGAGGCTACCCTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACCTCCCCGAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTTGT
CCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACC'TGTCCAGAACAGCTTTTTCGGA
TGCCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCT
GGAGGACCACAGCTTGTGAGGGCTGGCCAGCCTACAGGAACCTCTATCTCAACCACAACCAGCTCTACCGCATCGC
CCCCAGGGCCTTTTCTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAG
CCGTGGTTTGAATGCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
GAACCTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGAGATCTCCGACTATGC
CCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAGCTGGCCCCGGGTGCCAGGCGGGCCT
GGAACAGGTGCCCGGGCTCAAGTTCCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGC
CAACATGCTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGGCCCTGGT
GAACCTCCCCGAGCTGACCAAGCTGGACATCACCATAACCCACGGCTGTCTTTCATCCACCCCCGCGCCTTCCA
CCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCTCAGTGCCTTGCAACCAGCAGACGGTGGAGTC
CCTGCCCCAACC'TGCAGGAGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCTATCCGCTGGGCCAATGC
CACGGGCACCCGTGTCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGGCCCTCATCTCCCCACGAAGCTTCCCCCAAG
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTCTGATTGCCGGGCACTGGCCGAACCCGAACCCGAGATCTACTG
GGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCCT
GGAGCTGCGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGGCTGACAC
TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCG
GGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTACCCCCACCAACACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCCTCCTCCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTA
CAACATTAACCGCCTCCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCCACACCCCA
GTTGGCTTGTGTATGGGCCAGGACCAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGATCGTCTGGGCTCAT
TGCCATCCTGGCTCTCGCTGTCTTCTCTCTGGCAGCTGGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAA
GGGTGTGGGTGGGAGGCGGCCCTCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTTGT
GTCTGTCCCCCTCGTCTGCTTGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGGAGACACTGTTGCC
ACCATTTGTCTAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTTTACCAA
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGGC
CAAGACAGATGGGGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTCCCCATCTT
CTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGTGTCCCCGGGCTGCACCCCTTCTCTTC
TCTTTCTCTGTACAGTCTCAGTTGCTTGTCTTGTGCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC
CTCGGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAA
CGCTCATCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA
ATGTGTACCTCCCCCAACCCGATTCACTCTTTTCTCTGTTTTGTAAAAAATAAAAAATAATAACAATAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLILLQSNISIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILD MNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNO
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFI EPQSTLCAEPPDLQRLPVREVPPFREM TDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAE EAGLYT
CVAQNLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLP RSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

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FIGURE 87

GCAAGCCAAGGCGCTGTTTGAGAAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTTCATCCTCATCATCTGTACACCGTCTACTACGTGCACAA
CATCAAGTTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCCGTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGC
CAGCATTTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT
GGCTTCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTTACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGGCGTGACCTGCAGAACTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT
GCACCGCCTCACCTGCCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCTCCCTGCGGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCTTGCCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGAGGGGAGGCCCTAGCTTCTCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGGCTGGCCCCCTTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG
CTGCCACCAGAGGTCTTGGGACCTCACTTTAGTCTTGGTATTTATTTTTCTCCATCTCCACCTCCTTCATCC
AGATAACTTATACATTTCCCAAGAAAGTTCAAGCCAGATGGAAGGTGTTCAAGGAAAGGTGGGCTGCCCTTTTCCCC
TTGTCTTATTTAGCGATGCCGCCGGGCATTTAAACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCTCCAGCTGGA
AAGGCCAGGCCTGGAGCTTGCTCTTCAGTTTTTGTGGCAGTTTTAGTTTTTTGTTTTTTTTTTTTAAATCAAA
AAACAATTTTTTTTAAAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAAAAGAAAAAAAACCTTAAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTTCCCTTGAGCAAAGCAGCCAGACGT
TGAAGTGTGTTTTCTTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTCCTGGGGAGGGAGGTTTTTTTGTGTTTTTTTGGGTTTTTTTTTGGTGTCTTGTGTTTTCTTCTCCTCC
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGCTCCATTGCGACCTCCCTCCTCGTGCTGCCCTGCCTCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTCCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCACCTGGTCTTTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGTGCCCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGC
CTGGAGTGACACAGCCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAAGTTGTAGACTCGGTACAGTATCAATAAA
ATCTATAACAGAAAAAAA

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Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	0.45	0.50	0	1
Marital Status	0.60	0.49	0	1
Education	12.5	2.1	9	16
Income	3500	1500	1000	8000
Health Status	0.75	0.43	0	1
Employment	0.80	0.41	0	1
Stress Level	4.2	1.8	1	7
Life Satisfaction	5.8	1.5	3	7
Resilience	6.5	1.2	4	8
Optimism	6.2	1.4	4	8
Gratitude	6.8	1.3	4	8
Forgiveness	6.5	1.4	4	8
Self-Compassion	6.3	1.5	4	8
Emotional Regulation	6.7	1.2	4	8
Prosocial Behavior	6.9	1.1	4	8
Life Purpose	6.6	1.3	4	8
Meaning in Life	6.4	1.4	4	8
Existential Well-being	6.7	1.2	4	8
Transcendental Well-being	6.8	1.1	4	8
Overall Well-being	6.5	1.3	4	8

Transmembrane domain:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	Male	10.5	0	20
Marital status	Married	15.2	0	20
Education	High school	12.5	0	20
Occupation	Unemployed	18.5	0	20
Income	Low	15.5	0	20
Health status	Good	12.5	0	20
Stress level	High	18.5	0	20
Life satisfaction	Low	15.5	0	20
Resilience	Low	12.5	0	20
Optimism	Low	15.5	0	20
Self-efficacy	Low	12.5	0	20
Problem-solving	Low	15.5	0	20
Emotional regulation	Low	12.5	0	20
Social support	Low	15.5	0	20
Life events	High	18.5	0	20
Life goals	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	20
Life meaning	Low	15.5	0	20
Life purpose	Low	12.5	0	20
Life satisfaction	Low	15.5	0	20
Life meaning	Low	12.5	0	20
Life purpose	Low	15.5	0	20
Life satisfaction	Low	12.5	0	

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCCTTGGGTGATTCTCTGGATCTCCCCTGTTGATTCCGGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTAAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTGACGCG
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTG
GGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTTAAAAAATTGAT
TTGTTTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKS YKNLAFYWILKAGHMVP
SDQGD MALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACCTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTA CTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT
GGCCTGTAAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGTGTTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

0902736.0001

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWSVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

0900709E20660

[illegible][illegible]

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVSNRVPIPVWSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
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[illegible]

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	2.5	8	16
Income	3500	1500	1000	8000
Health status	75.0	25.0	50	100
Stress level	60.0	20.0	40	80
Life satisfaction	70.0	20.0	50	90
Work satisfaction	65.0	25.0	40	90
Family satisfaction	75.0	20.0	50	90
Community satisfaction	60.0	25.0	40	80
Overall satisfaction	68.0	22.0	45	85

Signal sequence:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCCTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCCTGCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCTTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCCCTCCCCGACCCGCCCCGAC
GGCCTCAGGCCCCCCTCCAAGGCATCAGGCCCCGCCCCAACGGCCTCATGTCCCCGCCCCCAC
GACTTCCGGCCCCGCCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTTATTCTCCAATTTCAATAAATTATTTATT
CTCCAAAAAAAAAA

090276-01001

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318

><subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

090270 0400
T00T00 0400

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTTATCCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCTTGACAGGGGCAAG
GGAATCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGCCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATAACCACTCAAAGGG
TGAAGAGGTGAGCTGTCCTCCTGTCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGGATTCTTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAATEASDSRKMGTTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSV
SGLNSGPGHVWGPLLGLLLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

0902736 95220650

General Information		Demographics		Clinical History		Physical Examination		Laboratory Studies		Imaging Studies		Treatment		Outcome			
Item	Value	Item	Value	Item	Value	Item	Value	Item	Value	Item	Value	Item	Value	Item	Value		
Age	45	Sex	Male	Chief Complaint	Headache	Location	Right side	Duration	3 days	Severity	7/10	Associated Symptoms	Nausea	Yes	Frequency	3 times	
Weight	75 kg	Height	175 cm	Medical History	Hypertension	Medications	Lisinopril	Current Medications	Lisinopril	Recent Changes	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
BMI	24.5	Family History	None	Social History	Smoker	Alcohol Use	Occasional	Stress Level	High	Work History	Software Engineer	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
BP	130/80	Education	Graduate	Exercise	Regular	Sleep	7 hours	Appetite	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
HR	72	Occupation	Software Engineer	Travel	Occasional	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
RR	18	Marital Status	Married	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
SpO2	98%	Religion	Christian	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
Temp	37.2	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
HR	72	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
RR	18	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
SpO2	98%	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
Temp	37.2	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
HR	72	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
RR	18	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
SpO2	98%	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
Temp	37.2	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
HR	72	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
RR	18	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
SpO2	98%	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
Temp	37.2	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
HR	72	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
RR	18	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
SpO2	98%	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
Temp	37.2	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
HR	72	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
RR	18	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal	Neurological Exam	Normal	Imaging	Normal
SpO2	98%	Language	English	Substance Use	None	Hydration	Normal	Energy	Normal	Weight Change	None	Physical Exam	Normal				

GTAACTGAAGTCAGGCTTTTCATTTTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAGTTATAGGTGGACGT
ACTTCTGTTGTTCTCCCTCTGCTTGGCTTTTTTCACATTAGCAGACCGGACTTAAGTCAACAAGATTATCTTTTCAT
CAAGGCAAGTTCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACTGAACAACAATGAATTGGAGACCATTCC
AAATCTGGGACCAGTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAA
TTTGCCCAACACACTCTCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGTATCCCCCAAGATGTTTAAACT
GCCCCAACTGCAACATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATCCAAAGCCCTTGG
TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAA
CATGGAAATTTTGAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCT
GCAGGAACCTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTTAAGCTTACTAAATAC
ACTGCACATTTGGGAACAACAGAGTCAGCTACATTTGCTGATTGCTCTCCGGGGCTTTCCAGTTTAAAGACTTT
GGATCTGAAGAACAAATGAAATTTCTGACTATTGAAGACATGAATGGTGGCTTTCTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCAGTGGTTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT
GCATTTAAATACATCAAGCCTTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAAACAACTT
TCAGAGCTTTGTAAATGCCAGTTGTGCCCATCTCAGCTGCCTAAAAGGAAGAAGCATTTTGTCTGTTAGCCCGA
TGGCTTTGTGTGTGATGATTTTCCCAAAACCCAGATCAGGTTTCAGCCAGAAACACAGTCGGCAATAAAGGTTT
CAATTTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGTCTGGAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCAC
CATCTTCCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTATCTCCAATCACTTTGGTTC
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCAT
CCGAGCTGGGGCCATGGCAGCTTGGAGTGTGCTGTGTTGGGCAACCCAGTCCCGCCCATAGCCTGGCAGAAGGA
TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGCTGTGATGCTGAGGATGACGTGTTCTTTATCGT
GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTACGCAAAATGC
AACTCTGACTGTCTTAGAAACACCATCATTTTTTGGCGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAAACAGC
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTTGGTGGT
AACCAGAGGGCACTTTTTGTCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAA
ATACACATGTGAGATGTCTAACACCTTTGGCCTGAGAGAGGAACCTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGAATGGGCCACTGTGGTGTCTGATCATAGC
CGTGGTTTGTGTGTGGTGGGCACGTCACCTGCTGTGGGTGGTTCATCATATACCACACAAGGCGGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCATCTCAGGGAAACGTT
AGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACCAGTTTGTCAATCTTCAGGTGCTGG
ATTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGGAAGCTGC
CACAGATCTGTTTCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAATGTGATGGCTCAGA
TCCTTTTGAACATATCATACAGTTTGCAGTCTTGACCAAGAACAGTTTAAATGAGGAACTATGAGCCCAAGTTA
CATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCTTCAGAAAGAAATCCTGCGAAGCGGAGCTTCAGTAATATATC
GTGGCCTTTCATAGTGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTG
TCTAAACAAGTCTCTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCCGTTGCTCGAGTAATTTCTTCATGGG
TACCTTTGGAAAAGCTCTCAGGAGACCTCACCATAGTGCCATTTCAGCTTTGGACAGCCATCAGAAATGTGACCC
AAGAGCCTTTTATTTGAAAGCTCATCTCTCCCAAGACTTGGACTTGGGTGAGGAGAGATGGGAAGAAAGGAC
AGATTTTCAGGAAGAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGATCCAAATTTTCAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTTATTTA
AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAATGCTTTATTTATACAGAT
GAACCAAAATTACAAAAAGTTATGAAAAATTTTATACCTGGGAATGATGCTCATATAAGAATACCTTTTTTAAACTA
TTTTTAACTTTGTTTTATGCAAAAAGTATCTACGTAATTAATGATATAAAATCATGATTTATTTTATGTAATTT
TTATAATGCCAGATTTCTTTTATGAAAAATGAGTTACTAAAGCAATTTAAATAATACCTGCCTTGTACCATTTT
TTAAATAGAAGTTACTTTCATTATATTTTTGCACATTATATTTAATAAAAATGTGTCAATTTTGAA

[illegible]

Signal sequence:

Transmembrane domain:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

1977-80 and 1981-82		1983-84		1985-86		1987-88		1989-90		1991-92		1993-94		1995-96		1997-98		1999-00		2001-02		2003-04		2005-06		2007-08		2009-10		2011-12		2013-14		2015-16		2017-18		2019-20		2021-22		2023-24		2025-26		2027-28		2029-30		2031-32		2033-34		2035-36		2037-38		2039-40		2041-42		2043-44		2045-46		2047-48		2049-50		2051-52		2053-54		2055-56		2057-58		2059-60		2061-62		2063-64		2065-66		2067-68		2069-70		2071-72		2073-74		2075-76		2077-78		2079-80		2081-82		2083-84		2085-86		2087-88		2089-90		2091-92		2093-94		2095-96		2097-98		2099-00		2101-02		2103-04		2105-06		2107-08		2109-10		2111-12		2113-14		2115-16		2117-18		2119-20		2121-22		2123-24		2125-26		2127-28		2129-30		2131-32		2133-34		2135-36		2137-38		2139-40		2141-42		2143-44		2145-46		2147-48		2149-50		2151-52		2153-54		2155-56		2157-58		2159-60		2161-62		2163-64		2165-66		2167-68		2169-70		2171-72		2173-74		2175-76		2177-78		2179-80		2181-82		2183-84		2185-86		2187-88		2189-90		2191-92		2193-94		2195-96		2197-98		2199-00		2201-02		2203-04		2205-06		2207-08		2209-10		2211-12		2213-14		2215-16		2217-18		2219-20		2221-22		2223-24		2225-26		2227-28		2229-30		2231-32		2233-34		2235-36		2237-38		2239-40		2241-42		2243-44		2245-46		2247-48		2249-50		2251-52		2253-54		2255-56		2257-58		2259-60		2261-62		2263-64		2265-66		2267-68		2269-70		2271-72		2273-74		2275-76		2277-78		2279-80		2281-82		2283-84		2285-86		2287-88		2289-90		2291-92		2293-94		2295-96		2297-98		2299-00		2301-02		2303-04		2305-06		2307-08		2309-10		2311-12		2313-14		2315-16		2317-18		2319-20		2321-22		2323-24		2325-26		2327-28		2329-30		2331-32		2333-34		2335-36		2337-38		2339-40		2341-42		2343-44		2345-46		2347-48		2349-50		2351-52		2353-54		2355-56		2357-58		2359-60		2361-62		2363-64		2365-66		2367-68		2369-70		2371-72		2373-74		2375-76		2377-78		2379-80		2381-82		2383-84		2385-86		2387-88		2389-90		2391-92		2393-94		2395-96		2397-98		2399-00		2401-02		2403-04		2405-06		2407-08		2409-10		2411-12		2413-14		2415-16		2417-18		2419-20		2421-22		2423-24		2425-26		2427-28		2429-30		2431-32		2433-34		2435-36		2437-38		2439-40		2441-42		2443-44		2445-46		2447-48		2449-50		2451-52		2453-54		2455-56		2457-58		2459-60		2461-62		2463-64		2465-66		2467-68		2469-70		2471-72		2473-74		2475-76		2477-78		2479-80		2481-82		2483-84		2485-86		2487-88		2489-9	
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GGGGAGAGGAATTGACCAIGTAAAGGAGACTTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG
 AAGGATGCAAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
 GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
 TAAACCAAGAGTTAGACCCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC
 CACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTACAAAGAAAAAAGTATGTTTCATTTTTCTC
 TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTTGGGGCTTTTTTAGTAGAAGTAAAGAACT
 GGTGTGGTGGTGTTCCTTTCTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAGAAAT
 TTTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
 TTTGTGCCTATGTTGATCAATAAATTGACGGATAATTTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTTTAAAT
 TTTTATCTCTTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAACACCTGGATTTCATCTGGATGTTGCT
 GTGATCAGTCTGAAATACAACGTGTTGAATCCGAGAAGGACCAACACAGGATAAATGAAATGTTGAACAAGAT
 GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGGCCCTAATTGACCCCTGCTTGTGGTGCT
 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA
 CCAGTTTCAGCAAGGTGATTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT
 GCTGAACCTCCATGAGAAGCAAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCATCTGGAATCCT
 ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGT
 GCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTTGCGCGCATAGACTTAGG
 GGAATTTGAAAAGACTTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGC
 CATGTGCAACCTTCGGGAAATCCCTTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTTCTGGGAATCA
 TTTATCTGCCATCAGGCCCTGGCTCTTTCCAGGGTTTGATGCACTTCAAAAACTGTGGATGATACAGTCCCAGAT
 TCAAGTGATTGAACGGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC
 ATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCAACCCCTTGAACCTG
 TAACGTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCGGTG
 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCATGCTATGCTCCGGT
 GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCCGGCCTCCACATC
 CCTGCATCTGTATCTTGGATTACTCCAAATGGAACAGTCAACATGACATGAGGGCGTACAAAGTCGGGATAGCTGT
 GCTCAGTGATGGTACGTAAATTTTCAAAATGTAACGTGTGCAAGATACAGGCATGACATGATGTTGGTGAAGTAA
 TTCCGTTGGGAATACTACTGCTTCAGCCACCTGTAATGTTACTGCAGCAACCACTACTCCTTTCTTACTTTTC
 AACCCTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGACCACAGATAACAATGTGGGTCCCACTCC
 AGTGGTCCAGTGGGAGACCACCAATGTGACCACCTCTCTCACACCAAGAGCACAAGGTGCACAGAGAAAACCTT
 CACCATCCAGTGACTGATATAAACAGTGGGATCCAGGAATGATGAGGTGATGAAGACTACCAAAATCATCAT
 TGGGTGTTTTGTGGCCATCACACTATGGCTGCAGTATGCTGGTCAATTTCTACAAGATGAGGAAGCAGCACCA
 TCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC
 CATGGAAGGCCACTGCCCATGCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
 CAACCAACAACAACAGTTAAACACAATAAATTCATAACACAGTTTCAGTGCATGAACCGTTATTGATCCGAATGAA
 CTTAAGAGCAATGTACAAGAGACTCAAACTTAAACACTTTACAGAGTTACAAAAACAAACAATCAAAAAA
 GACAGTTTATTAATAAATGACACAAATGACTGGCTTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAA
 AAAAGAAAAAGAAATTTATTTATTAATAAATCTATTGTGATCTAAAGCAGCAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGA FEGLSNLRYLNLMCNLREIPNLTPLIKDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVSGN
TTASATLNVTAATTTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNTTSLTPQ
STRSTEKTFTIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

090276-01001

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA
TGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACGCGACCGC
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGCCGGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGGGGGTTGGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGCGTCCGGGGGAACCTCGGGCAGCCCTCTGGGGTAGCCGCC
GAGCGCCCATGCCCCACTACCTGCCGCTGCCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT
CCCGAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCC
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
GTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATTTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACTGGGTATTTTGACAATTTGGCCAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCAACTGCAA
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTTCAAGGCCCTTGGTGCTCTGAAGTCT
CTGAAAATGCAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTGGGGGGCTGAGCAACATGGAAATTTTG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCAT
CTCAGCAAAATGCCATCAACAGGATCAGCCCTGATCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGCACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATACACTGCACATTTGGG
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTTCTTGGACTATTGAAGACATGAATGGTGCTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAATTGCATTTAAATACA
TCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCAAGCTGGGTGGCGGAAACAACCTTTCAGAGCTTTGTA
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTGTGCTTAGCCAGATGGCTTTGTGTGT
GATGATTTTCCAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTTGTCTGGAAAAAGACAATGAACACTGCATGAT
GCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCACCATCTTCCGGCTG
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCCAATCACTTTGGTTTCACTCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA
GAGGACATTTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTAGCAAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGCCGCTCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAAGTGGCCAAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC
TTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACACATGTGAG
ATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTGCTGATCATAGCCGTGGTTTGTGT
GTGGTGGGCACGTCACCTCGTGTGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC
AACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCATCTCAGGGAACGTTAGCTGACAGGCAG
GATGGGTACGTGCTTTCAGAAAGTGGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTT
CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACA
TATCATACAGGTTGCAGTCTTGACCCAAGAACAGTTTAAATGGACCACTATGAGCCAGTTACATAAAGAAAAAG
GAGTGCTACCCATGTTCTCATCTTTCAGAAAGTCTGCGAACCGGAGCTTCAGTAATATATCGTGGCCTTCACAT
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
TCTTTAGATTTTAGTGCAAAATCCAGAGCCAGCGTCGGTTGCCCTCGAGTAATTCTTTCATGGGTACCTTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTAT
TTGAAAGCTCATTCTTCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA
GAAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGCTTAACTACTACCTCAAGTGAACCTTTTATTTAAAGAGAGAGAAT
CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGATGAACCAAAATTAC
AAAAAGTTATGAAAATTTTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTG
TTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTTATAATGCCAGA
TTCTTTTTTATGGAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAAATAGAAGTT
ACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09902736-071001

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRISAIPPKMFKLPLQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDWEFC
QKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSOMK
KLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNE LLHDAEMENY AHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF
FAAGNQLLIIVDSVDSDAGKYTCEMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
TVGVVIIAVVCCVVGTS LVVVIIYHTRRRNEDCSITNTDETNL PADIPSYLSSQGT LADRQ
DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDPFETYHTGCSPDPRTVLM DHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEEHICTFKQTL ENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

Variable	Mean	SD	Min	Max
Age	38.5	12.5	18	65
Gender	50%	50%	0	100
Marital status	75%	25%	0	100
Education	12.5	2.5	8	16
Income	3500	1500	1000	8000
Occupation	15%	85%	0	100
Health status	70%	30%	0	100
Stress level	65%	35%	0	100
Life satisfaction	75%	25%	0	100
Resilience	60%	40%	0	100
Optimism	70%	30%	0	100
Gratitude	75%	25%	0	100
Forgiveness	65%	35%	0	100
Empathy	70%	30%	0	100
Compassion	75%	25%	0	100
Kindness	70%	30%	0	100
Generosity	75%	25%	0	100
Patience	70%	30%	0	100
Humility	75%	25%	0	100
Modesty	70%	30%	0	100
Shyness	65%	35%	0	100
Introversion	60%	40%	0	100
Extroversion	40%	60%	0	100
Sensitivity	70%	30%	0	100
Emotionality	65%	35%	0	100
Impulsivity	55%	45%	0	100
Risk-taking	45%	55%	0	100
Adventurousness	50%	50%	0	100
Curiosity	60%	40%	0	100
Openness	65%	35%	0	100
Conscientiousness	70%	30%	0	100
Agreeableness	75%	25%	0	100
Neuroticism	40%	60%	0	100
Stability	60%	40%	0	100
Control	65%	35%	0	100
Order	70%	30%	0	100
Discipline	75%	25%	0	100
Perseverance	70%	30%	0	100
Endurance	75%	25%	0	100
Stamina	70%	30%	0	100
Strength	75%	25%	0	100
Power	70%	30%	0	100
Influence	75%	25%	0	100
Authority	70%	30%	0	100
Leadership	75%	25%	0	100
Management	70%	30%	0	100
Organization	75%	25%	0	100
Planning	70%	30%	0	100
Preparation	75%	25%	0	100
Provision	70%	30%	0	100
Protection	75%	25%	0	100
Preservation	70%	30%	0	100
Perpetuation	75%	25%	0	100
Perfection	70%	30%	0	100
Perfectionism	75%	25%	0	100
Perfectionist	70%	30%	0	100
Perfectionistic	75%	25%	0	100
Perfectionism	70%	30%	0	100
Perfectionist	75%	25%	0	100
Perfectionistic	70%	30%	0	100
Perfectionism	75%	25%	0	100
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Perfectionistic	75%	25%	0	100
Perfectionism	70%	30%	0	100
Perfectionist	75%	25%	0	100
Perfectionistic	70%	30%	0	100
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Perfectionistic	75%	25%	0	100
Perfectionism	70%	30%	0	100
Perfectionist	75%	25%	0	100
Perfectionistic	70%	30%	0	100
Perfectionism	75%	25%	0	100
Perfectionist	70%	30%	0	100
Perfectionistic	75%	25%	0	100
Perfectionism	70%	30%	0	100
Perfectionist	75%	25%	0	100
Perfectionistic	70%	30%	0	100
Perfectionism	75%	25%	0	100</

CAAAACCTTGCCTCGCGGAGAGCGCCACGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC
 TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
 CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCCTATCCCTCCTTTATATA
 GAAACCTTCCACACTTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG
 GCCACAGCATTCGAGTTTACAGATTTTACAGATACCAAATGCGAAGGCGAGGAGGCAGAACAGCCCTGCCCTGGT
 TCCATCAGCCCTGGCGCCAGCGCATCTGACTCGGCACCCCTGTGAGGCACCATGGCCAGCCAGGCGGGTGTCTGC
 TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGGCGTGAGGGCCCGAGATTTGGCCGAA
 GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGTGGTACTGAGCCCTGAGG
 AGCCCCGGGCTGGCCAGCCGCGGTGAGCTGCCCCCGAGACTGTGCCCTGTTCCAGGAGGGCGTCTGTGGACTGTG
 GCGGTATTGACCTGCGTGAGTTCCCGGGGGACCTGCCCTGAGCACACCAACCACCTATCTCTGCAGAACCAACCAGC
 TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGGTGCACCCGGCTGGAGACACTGAACCTGCAAAAACAACCGCCTGA
 CTTCCTCGAGGGCTCCCAGAGAAGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCCAATAACAAGC
 TGACCTTTGGCACCCCGCTTCTTCCGCAACCGCCCTGATCAGTGTGGACTTTGTGTGCCAACTATCTCACCAAGATCT
 ATGGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC
 TGCCCGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCTCATCTGTCCAGCAACTTCTTGCGCCACGTGC
 CCAAGCACCTGCCGCCCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT
 TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACTACCTGACTGACGAGGGCCTGGACAACGAGA
 CTTCTGGAAGCTCTCCAGCTGGAGTACCTGGATCTGTCCAGCAACCACTGTCTCGGTCCTCCAGCTGGGCTGC
 CGCGCAAGCTGGTGTCTGTCTGCACCTTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGTGACCCCATCC
 GCAGCCTGGAGTACCTGTCTGTCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC
 TCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCTGCCAGTGGCCTGCCCTCGCCGCTGTGC
 GCACCTCATGATCCTGCACAACCAGATCACAGGCAATTGGCCGCGAAGACTTTGCCACCACCTACTTCTTGGAGG
 AGCTCAACCTCAGCTACAACCGCATCACAGCCCAAGCTGCACCGCGACCGCCTTCCGCAAGCTGCGCCTGTCTGC
 GCTCGCTGGACCTGTGCGGCCAACCGCTGCACACGCTGCCACTTGGCTGCCCTCGAAATGTCCATGTGTCTGAAG
 TCAAGCGCAATGAGCTGGCTGCCCTTGGCACGAGGGGCGCTGCGCGGATGGCTCAGCTGCGTGAGCTGTACTCTCA
 CCAGCAACCAGCTGCGCAGCCGAGCCCTGGGCCCCCGTGCCCTGGGTGGACCTCGCCCATCTGCAGCTGTCTGGACA
 TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACTTGCAGAACAAACA
 AGATTAGTGCGGTGCCCGCCAATGCCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAAGC
 TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT
 TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAGGAGGAGGAGG
 AGGAAGAGGAACAAGATAGTACCAAGGTGATGCAGATGTGACTAGGATGATGAGCCCGCGACTCTTTTCTGC
 AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTCTCACACAGACACCCAGCTGCACATGAGGCA
 TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCCACGGCCAGACACATGC
 ACACACATCACACCTTCAAACACCCAGCTCAGCCACACACAACCTACCTTCAAACACCACACAGTCTCTGTACAC
 CCCCCTACCGCTGCCACGCCCCCTGGAATCATGCAGGGAAGGCTGTGCCCTGCCCTGGCACACACAGGCACCCA
 TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCAACACACACACATGCACAAGTCATGTGCGAA
 CAGCCCTTCAAAGCCTATGTCACAGACAGTCTTGGCCACAGCAGAATCAGCCATAGCAGCTCGCGCTGTGCCCT
 GTCCATCTGTCCGTCCGTTCCTTGGAGAAGACACAAGGGTATCCATGCTGTGTGGCCAGGTGCTGCTGCCCTCT
 GGAACCTCAAAAAGCTGGCTTTTATTTCTTTCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC
 TGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
 CAGGCACTTTTCCAATGGGCAAGCCCACTGGAGGCGAGATGGGAGAGCCCCCTGGGTGCTGTGGGGCCTTGGGG
 CAGGAGTGAAGCAGAGGTTGATGGGGCTGGGCTGAGCCAGGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT
 GTTCTTCAGGCTGTGGGGAGGTTCCGGGTGCCCTTATTTTATTTCTTTCTTAAGGAAAAAATGATAAAAAAT
 CTCAAAGCTGATTTTCTTGTATATAGAAAACTAATAAAGCACTATCCCTATCCCTGCAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPRPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSP ENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFFPGDLP
EHTNHLSSLQNNQLEKIYPEELSRHRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

Variable	Mean	SD	Min	Max
Age	38.5	10.5	25	55
Gender	1.0	0.0	0	1
Marital status	1.0	0.0	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	6000
Health status	1.0	0.0	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	1.0	1.0	0	3
Stress level	2.0	1.0	1	3
Sleep quality	1.0	1.0	0	2
Dietary habits	1.0	1.0	0	2
Work-life balance	1.0	1.0	0	2
Family support	1.0	1.0	0	2
Community involvement	1.0	1.0	0	2
Personal growth	1.0	1.0	0	2
Life satisfaction	1.0	1.0	0	2
Overall well-being	1.0	1.0	0	2

Variable	Mean	SD	Min	Max
Age	38.5	10.5	25	55
Gender	1.0	0.0	0	1
Marital status	1.0	0.0	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	6000
Health status	1.0	0.0	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	1.0	1.0	0	3
Stress level	2.0	1.0	1	3
Sleep quality	1.0	1.0	0	2
Dietary habits	1.0	1.0	0	2
Work-life balance	1.0	1.0	0	2
Family support	1.0	1.0	0	2
Community involvement	1.0	1.0	0	2
Personal growth	1.0	1.0	0	2
Life satisfaction	1.0	1.0	0	2
Overall well-being	1.0	1.0	0	2

FIGURE 110

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDDVVKQIIRCQCPSPLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKNGTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTLRTPLPPTTPTTGLTTIAPAASTPPGGITVDN
RVQTDPPQKPRGDFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAKAPGG
KAARLVLPGLRLMHSGDLCLSFHVKVTGLHSGTLQVVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 110

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCCTTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACCTTTCTTTCTTTTGCAACAGGTGCTTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTGAGGCCCTCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCA
GAAGATAACAAGTACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCCTGTGAGTGAATGGAAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCAGACAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTGATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG
ATTCOAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTCAGCACATCCCTGCCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG
GCTAAACAGTACATTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA
TGCAGAATAGAGGCATTTATGCAAATGAACTGCAGGTTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTTCACATATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTTACATTGTTGATTTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAACCTATGCCTTCTCTTTTTTTTCAATCACC
AGTAGTATTTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA
TTTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGCTTTTAAAAAAAAAAAAA

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FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTSLASQ
KIQVTVDDPVTKPVVQIHPSPGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVITTSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

0390273-071001

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	2.5	8	16
Income	3500	1500	1000	8000
Occupation	2.5	1.5	1	5
Health status	75.0	25.0	50	100
Stress level	60.0	20.0	40	80
Life satisfaction	70.0	20.0	50	90
Resilience	65.0	15.0	50	80
Optimism	75.0	15.0	60	90
Gratitude	80.0	10.0	70	90
Forgiveness	70.0	15.0	50	90
Empathy	75.0	15.0	60	90
Compassion	70.0	15.0	50	90
Kindness	75.0	15.0	60	90
Generosity	70.0	15.0	50	90
Patience	75.0	15.0	60	90
Humility	70.0	15.0	50	90
Modesty	75.0	15.0	60	90
Shyness	60.0	20.0	40	80
Introversion	50.0	50.0	0	100
Extroversion	50.0	50.0	0	100
Sensitivity	60.0	20.0	40	80
Emotionality	50.0	50.0	0	100
Stability	50.0	50.0	0	100
Neuroticism	40.0	30.0	10	70
Conscientiousness	60.0	20.0	40	80
Agreeableness	70.0	15.0	50	90
Openness	65.0	15.0	50	80
Curiosity	70.0	15.0	50	90
Imagination	65.0	15.0	50	80
Adaptability	70.0	15.0	50	90
Flexibility	65.0	15.0	50	80
Resilience	65.0	15.0	50	80
Optimism	75.0	15.0	60	90
Gratitude	80.0	10.0	70	90
Forgiveness	70.0	15.0	50	90
Empathy	75.0	15.0	60	90
Compassion	70.0	15.0	50	90
Kindness	75.0	15.0	60	90
Generosity	70.0	15.0	50	90
Patience	75.0	15.0	60	90
Humility	70.0	15.0	50	90
Modesty	75.0	15.0	60	90
Shyness	60.0	20.0	40	80
Introversion	50.0	50.0	0	100
Extroversion	50.0	50.0	0	100
Sensitivity	60.0	20.0	40	80
Emotionality	50.0	50.0	0	100
Stability	50.0	50.0	0	100
Neuroticism	40.0	30.0	10	70
Conscientiousness	60.0	20.0	40	80
Agreeableness	70.0	15.0	50	90
Openness	65.0	15.0	50	80
Curiosity	70.0	15.0	50	90
Imagination	65.0	15.0	50	80
Adaptability	70.0	15.0	50	90
Flexibility	65.0	15.0	50	80
Resilience	65.0	15.0	50	80
Optimism	75.0	15.0	60	90
Gratitude	80.0	10.0	70	90
Forgiveness	70.0	15.0	50	90
Empathy	75.0	15.0	60	90
Compassion	70.0	15.0	50	90
Kindness	75.0	15.0	60	90
Generosity	70.0	15.0	50	90
Patience	75.0	15.0	60	90
Humility	70.0	15.0	50	90
Modesty	75.0	15.0	60	90
Shyness	60.0	20.0	40	80
Introversion	50.0	50.0	0	100
Extroversion	50.0	50.0	0	100
Sensitivity	60.0	20.0	40	80
Emotionality	50.0	50.0	0	100
Stability	50.0	50.0	0	100
Neuroticism	40.0	30.0	10	70
Conscientiousness	60.0	20.0	40	80
Agreeableness	70.0	15.0</		

GCAAGCGGCGGAAATGCGGCCCTCCGGGAGTCTTGCAGATTCCCTGGCAGTCTCTGGTGCTGTT
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCGTGGTGCCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTTACAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATAACCCATAACCTTCAAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGTATAAAAAACAGAAGATTGATCATTTTGTTTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCAATTAAATTGAAGAGTCTA
CATTACAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAATTTACATTTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTCAGTGACAATTTCTGGTCTTTTTTAGAGGTATATTCCAAATTTCTTGT
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATT
CAACAAAGTTTGATTTTTCTCTTGATTTTTCTTACTTACTATGGGTACATTTTTTATTTTT
CAAATTGGATGATAATTTCTTGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGT
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAAT
TTGGCCACTTTTTTACAGATTTTACATCATTCTTGCTGAACTTCAACTTGAAATTGTTTTTT
TTTCTTTTTGGATGTGAAGGTGAACATTCCTGATTTTTGTCTGATGTGAAAAAGCCTTGGA
TTTTACATTTTGAAAATTCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAG
CATCTTCTTGATATATGTCTTAAATGTATTTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTTTAAATAATAACATTTTATATTTTTTAAAGACAA
ACTTCATATTATCTGTGTTCTTCTGACTGGTAATATTGTGTGGGATTTACACAGGTAAAA
GTCAGTAGGATGGAACATTTTGTGATTTTTTACTCCTTAAAGAGCTAGAAATACATAGTTTT
CACCTTAAAGAAGGGGGAAAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTTCTGTAATGTCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT
AAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSI EPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSE
EEAESKEGTNKDFPQNAIRQRS LGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

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FIGURE 115

CGGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCTTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTTTGGTGTCTTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
GAGGGGAACCTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
GGCCGCTCGGCCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGGCCTGGAGCTCACCCGCCGCTGCTC
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTGGG
GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
TCGTGAGGTACTACGATGTCTGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCACTGTGCGCCAGCTA
CCGGGTTTTCAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG
GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCCTGCCC
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGTTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTTGACATCCTTTTCTGTCTTCCCCTTCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTCTTATCAGGCT
GATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTTCCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTTAT
GGCATTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSVCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP
TDEDEIGAALMRLQDTYRLDPGTISRGEIPGTTYQAMLSVDDCFGMGRSAYNEGDYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPSHERAGGNLR
YFEQLLEEEREKTLTNQTEAELATPEGIYERPVDYLPERDVYESLCRGEVVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGECDYR
TRHAACPVLVGCKWVSNKWFHERGQEFRLPCGSTVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

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FIGURE 117

GCAGTATTGAGTTTACTTCCTCCTCTTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTTTGGCTGGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTTGGGGATGCTGGTCTCTGGAAGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCC
CAGGTTCTCTGGTTAAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGGCACCCACCTGGCAGGGCCTACCACC**ATG**CGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGGTGAGCCTGAGCCTCCTGCGGGTTTCTGGATCCAGGGGGAGGGAGAAG
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA
CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGCGGGGGG
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGATGAGCGGCCCGCCTGGCTCATGTGAGAGCCCTGC
GCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTTCATCATGCAGGATGACACATATGTGCAGGCCC
CCCGCCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTATTG
GCGCAGGCGAGCAGGCCCCGTACTGTCTGAGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCTGC
GGCCACATCTGGATGGCTGCGGAGGAGACATTCTCAGTGCCCGTCTTGACGAGTGGCTTGGACGCTGCCTCATTG
ACTCTCTGGGCGTGGCTGTGTCTCACAGCACCAGGGGCGAGTATCGCTCATTGAACTGGCCAAAATAGGG
ACCCTGAGAAGGAAGGAGCTCGGCTTTCTGAGTGCCTTCGCCGTGCACCCTGTCTCCGAAGGTACCCCTCATGT
ACCGGCTCCACAAAAGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAACCTGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCA
CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCTGTGCAGATGGGG
CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCGTATCAGCCCCGCTGCGCTTCCAGAAGCAGCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCAC
GGGGCATGGAGTACACCCCTGGACCTGCTGTGGAAATGTGTGACACAGCGTGGGCACCGGCGGGCCCTGGCTCGCA
GGGTGAGCCTGTGCGGCCACTGAGCCGGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC
AGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCTCGAGGCGTTTGCAGCCAATGTCC
TGGAGCCACGAGAACATGCATTGCTCACCCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG
ACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCTGTGGACACTCTCT
TCTTCCTTACCACCGTGTGGACAAGGCTGGGGCCCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT
GGCAGGCTTCTTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTCAACACAGAGATCACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTCCTGGTGCTGACCCCTCCCGGGGGGCTCCTATAGGGGGGAGATTTG
ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGGCCGAGCCCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCTCCGGTTCTCAGGGCTCC
ACCTCTTTCGGGCCGTAGAGCCAGGGCTGGTGCAAGATTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG
AACTCTACCACCGTGCCGCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTCTTTG
AGCAGGAGCAGGCCAATAGCACT**TAG**CCCGCTGGGGGCCCTAACCTCATTACCTTTCTTTGTCTGCCTCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAATGTTATTAA
ACATGTCTTCTGCC

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Variable	Mean	SD	Min	Max
Age (years)	35.2	12.5	18	65
Gender (Male/Female)	50/50			
Marital status (Married/Single)	60/40			
Education (High school/College/Postgraduate)	30/40/30			
Occupation (Student/Professional/Unemployed)	20/40/40			
Family size (1-3/4-6/7-9)	30/40/30			
Religious affiliation (Muslim/Christian/Other)	50/50			
Health status (Healthy/Chronic disease/No response)	40/40/20			
Income (Low/Medium/High)	30/40/30			
Urban/rural (Urban/Rural)	50/50			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)	30/40/30			
Season (Spring/Summer/Autumn/Winter)	25/25/25/25			
Weather (Sunny/Cloudy/Rainy)	30/40/30			
Time of day (Morning/Afternoon/Evening)				

Signal sequence:

Transmembrane domain:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTG
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGCTTAAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGCGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTTCTTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTTTAAATGAGGGTGGTTTTTTTTCTTTAAAACACATGAACATTGTAAATG
TGTTGGAAAGAAGTGTTTTAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTTGCTGATTGGTT
AAAAAATTTTAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCTTCTCAAATGTACAATAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

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FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

090273-0700
T00T70"9E720650

FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAGAAACAAAAAACCAAAGAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA
AACCTAAAATGAGAGAGTTTTTTTATTGGACTGTGAGACCAGGTTGTGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAAATAAGTAGTTTTTAAATGTTAAAAAAAAAAAAA
AAA
AAAAA

090276-07100
T00T20 9E20660

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	2.5	8	16
Income	3500	1500	0	8000
Occupation	2.5	1.5	0	5
Health status	75.0	25.0	0	100
Life satisfaction	60.0	20.0	0	100
Stress level	45.0	15.0	0	100
Work-life balance	55.0	18.0	0	100
Family support	70.0	22.0	0	100
Community involvement	65.0	20.0	0	100
Personal growth	50.0	15.0	0	100
Financial stability	60.0	18.0	0	100
Emotional well-being	65.0	20.0	0	100
Physical health	70.0	22.0	0	100
Mental health	60.0	18.0	0	100
Social relationships	65.0	20.0	0	100
Work satisfaction	55.0	15.0	0	100
Life goals achievement	50.0	12.0	0	100
Overall quality of life	60.0	15.0	0	100

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACGTCTTGCATCATTACGGATTTCG
AGACAAGTGACCCAGGATCGAGTGGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTGACAACAAA
TTTCAGGGAGACTTGGCGGGTCTGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCTTTGCTCGAAATGACCGCAAGGAAATTTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCCTGCCACGGATT
CCAGAGCCAATCCCAGATTTTCGCAATTTCTTTTCACTTAAACTCTGAAACAGGCAC'TTTGGTGTTCCTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCTTGTCTGTAAGTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTTG
TGATCTGAAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGTCTACGTAACGCCCGTGTGGGGGCTGTGAAGCCAGCATGTTTACCCTGGTCTGTT
CAGCAGCCACGACAGCACCATTGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTTCATCGGCCCACAGACACCACCGAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTGTCAGTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTTTGTAAAAACAACCAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGATTAAAGGAAA
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TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTTCT
CACACAAGTTTGTAGCTTTTTCACAAGGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGGTTCGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT
CCCCTGTTCTCTTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG
TGAAACGCCTGAATCAAAAGCAGTTTCTAATTTTGACTTTAAATTTTTTTCATCCGCCGAGACACTGCTCCCATT
TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTTGCCGAGGCGCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACAGCTCCAGCCTCCT
TCTTGGTTGTATAGTATAGGGTAGCCTTATGCCCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTTGGCATTGTGTTAAC
CTCATTTATAAAAGCTTCAAAAAAACCCA

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Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	2.5	8	16
Income	3500	1500	1000	8000
Occupation	2.5	1.5	1	5
Health status	75.0	25.0	50	100
Stress level	60.0	20.0	40	80
Life satisfaction	70.0	20.0	50	90
Resilience	65.0	25.0	40	90
Optimism	75.0	20.0	50	100
Emotional stability	60.0	25.0	30	90
Self-efficacy	70.0	20.0	50	90
Perceived social support	65.0	25.0	40	90
Coping strategies	55.0	20.0	30	80
Problem-solving skills	60.0	25.0	35	85
Emotional regulation	65.0	20.0	40	90
Resilience training	70.0	25.0	45	95
Stress management	65.0	20.0	40	90
Life skills training	75.0	25.0	50	100
Emotional support	60.0	20.0	35	85
Problem-solving training	70.0	25.0	45	95
Emotional regulation training	65.0	20.0	40	90
Resilience training	75.0	25.0	50	100
Stress management training	65.0	20.0	40	90
Life skills training	75.0	25.0	50	100
Emotional support training	60.0	20.0	35	85
Problem-solving training	70.0	25.0	45	95
Emotional regulation training	65.0	20.0	40	90
Resilience training	75.0	25.0	50	100
Stress management training	65.0	20.0	40	90
Life skills training	75.0	25.0	50	100
Emotional support training	60.0	20.0	35	85
Problem-solving training	70.0	25.0	45	95
Emotional regulation training	65.0	20.0	40	90
Resilience training	75.0	25.0	50	100
Stress management training	65.0	20.0	40	90
Life skills training	75.0	25.0	50	100
Emotional support training	60.0	20.0	35	85
Problem-solving training	70.0	25.0	45	95
Emotional regulation training	65.0	20.0	40	90
Resilience training	75.0	25.0	50	100
Stress management training	65.0	20.0	40	90
Life skills training	75.0	25.0	50	100
Emotional support training	60.0	20.0	35	85
Problem-solving training	70.0	25.0	45	95
Emotional regulation training	65.0	20.0	40	90
Resilience training	75.0	25.0	50	100
Stress management training	65.0	20.0	40	90
Life skills training	75.0	25.0	50	100
Emotional support training	60.0	20.0	35	85
Problem-solving training	70.0	25.0	45	95
Emotional regulation training	65.0	20.0	40	90
Resilience training	75.0	25.0	50	100
Stress management training	65.0	20.0	40	90
Life skills training	75.0	25.0	50	100
Emotional support training	60.0	20.0	35	85
Problem-solving training	70.0	25.0	45	95
Emotional regulation training	65.0	20.0	40	90
Resilience training	75.0	25.0	50	100
Stress management training	65.0	20.0	40	90
Life skills training	75.0	25.0	50	100
Emotional support training	60.0	20.0	35	85
Problem-solving training	70.0	25.0	45	95
Emotional regulation training	65.0	20.0	40	90
Resilience training	75.0	25.0	50	100
Stress management training	65.0	20.0	40	90
Life skills training	75.0	25.0	50	100
Emotional support training	60.0	20.0	35	85
Problem-solving training	70.0	25.0	45	95
Emotional regulation training	65.0	20.0	40	90
Resilience training	75.0	25.0	50	100
Stress management training	65.0	20.0	40	90
Life skills training	75.0	25.0	50	100
Emotional support training	60.0	20.0	35	85
Problem-solving training	70.0	25.0	45	95
Emotional regulation training	65.0	20.0	40	

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><subunit 1 of 1, 310 aa, 1 stop
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MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPAVPVGMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTA VHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIIGGIIGG
VLVVLAVLALITLGICAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Signal peptide:

Transmembrane domain:

N-glycosylation sites.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267